

#2

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/892,942

DATE: 10/16/2001

TIME: 14:13:26

Input Set : N:\Crf3\RULE60\09892942.txt

Output Set: N:\CRF3\10162001\I892942.raw

4 <110> APPLICANT: Shyjan, Andrew W.
6 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION
7 AND TREATMENT OF TUMOR PROGRESSION
9 <130> FILE REFERENCE: 07334/004005
11 <140> CURRENT APPLICATION NUMBER: 09/892,942
12 <141> CURRENT FILING DATE: 2001-06-27
14 <150> PRIOR APPLICATION NUMBER: 09/181,030
15 <151> PRIOR FILING DATE: 1998-10-27
17 <150> PRIOR APPLICATION NUMBER: US 08/862,442
18 <151> PRIOR FILING DATE: 1997-05-23
20 <150> PRIOR APPLICATION NUMBER: US 08/623,679
21 <151> PRIOR FILING DATE: 1996-03-29
23 <160> NUMBER OF SEQ ID NOS: 10
25 <170> SOFTWARE: FastSEQ for Windows Version 3.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 186
29 <212> TYPE: DNA
30 <213> ORGANISM: Mus musculus
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33 ggtgctggag tacctcatgg gcggtgccta ccgctgcaac tacactcgga aaagcttccg 60
34 gactctctac aacaacttgt ttggccctaa gagggtagag ctcagcagac acacagtgtc 120
35 ctgtgcctcc cagagtaaca tgtggttcc tcatgtgctt ccccaaaagc ccacctgtgc 180
36 agaatg 186
38 <210> SEQ ID NO: 2
39 <211> LENGTH: 2729
40 <212> TYPE: DNA
41 <213> ORGANISM: Mus musculus
43 <220> FEATURE:
44 <221> NAME/KEY: CDS
45 <222> LOCATION: (321)...(1946)
47 <400> SEQUENCE: 2
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49 ggatagagaa gacattttgc aaaagggaat gcatctttgt aattcccagt acaaaagacc 120
50 ctaacagatg ttgctgtggt cagctcacta accagcacat ccccccttg ccgagtggg 180
51 ctcccagcac aacaggagag gacaccaagc aggcagacac gcagtccggg aaatggctg 240
52 tcagcaaaca caccagagc tacccaacag actcctatgg gattcttgaa ttccagggtg 300
53 ggggttactc caataaagcc atg tac atc cga gtc tcc tac gac acc aag cca 353
54 Met Tyr Ile Arg Val Ser Tyr Asp Thr Lys Pro
55 1 5 10
57 gat tcc ctg ctc cac ctc atg gtg aag gac tgg cag ctg gag ctc ccg 401
58 Asp Ser Leu Leu His Leu Met Val Lys Asp Trp Gln Leu Glu Leu Pro
59 15 20 25
61 aag ctc ttg ata tct gtg cac gga ggc ctc caa agc ttc gag atg cag 449
62 Lys Leu Leu Ile Ser Val His Gly Leu Gln Ser Phe Glu Met Gln
63 30 35 40
65 tcc aaa ctg aag cag gtg ttt ggg aaa ggt ctg atc aag gct gcc atg 497
66 Ser Lys Leu Lys Gln Val Phe Gly Lys Gly Leu Ile Lys Ala Ala Met

ENTERED

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67	45	50	55	
69	acc acg ggg gcg tgg atc ttc acc ggg ggt gtg agc act ggt gtc gtc	545		
70	Thr Thr Gly Ala Trp Ile Phe Thr Gly Gly Val Ser Thr Gly Val Val			
71	60	65	70	75
73	agc cat gtg ggg gat gcc ttg aaa gac cac tcc tcc aag tcc aga ggc	593		
74	Ser His Val Gly Asp Ala Leu Lys Asp His Ser Ser Lys Ser Arg Gly			
75	80	85	90	
77	cgg ctc tgt gct ata gga att gct ccc tgg ggc atg gtg gag aac aag	641		
78	Arg Leu Cys Ala Ile Gly Ile Ala Pro Trp Gly Met Val Glu Asn Lys			
79	95	100	105	
81	gaa gac ctg att gga aaa gat gta aca aga gtc tat cag acc atg tcc	689		
82	Glu Asp Leu Ile Gly Lys Asp Val Thr Arg Val Tyr Gln Thr Met Ser			
83	110	115	120	
85	aac cct ctg agc aag ctc tct gtg ctc aac aat tcc cac act cac ttc	737		
86	Asn Pro Leu Ser Lys Leu Ser Val Leu Asn Asn Ser His Thr His Phe			
87	125	130	135	
89	atc ttg gct gac aac ggc acc ctg ggc aag tat ggt gct gag gtg aag	785		
90	Ile Leu Ala Asp Asn Gly Thr Leu Gly Lys Tyr Gly Ala Glu Val Lys			
91	140	145	150	155
93	ctt cga aga cag ctg gaa aaa cac atc tcc ctg cag aag atc aac aca	833		
94	Leu Arg Arg Gln Leu Gly Lys His Ile Ser Leu Gln Lys Ile Asn Thr			
95	160	165	170	
97	agg ctg ggc cag ggt gta cct gtc gtg ggc cta gtg gta gaa ggt ggt	881		
98	Arg Leu Gly Gln Gly Val Pro Val Val Gly Leu Val Val Glu Gly Gly			
99	175	180	185	
101	cct aac gtg gtt tct atc gtc ctg gag tat ctc aaa gaa gac cct cct	929		
102	Pro Asn Val Val Ser Ile Val Leu Glu Tyr Leu Lys Glu Asp Pro Pro			
103	190	195	200	
105	gtc cct gtg gtg gtt tgc gat ggc agt gga cgt gcc tct gac att ttg	977		
106	Val Pro Val Val Val Cys Asp Gly Ser Gly Arg Ala Ser Asp Ile Leu			
107	205	210	215	
109	tcc ttc gca cac aaa tac tgc gac gaa gga gga gtc ata aac gag tcc	1025		
110	Ser Phe Ala His Lys Tyr Cys Asp Glu Gly Gly Val Ile Asn Glu Ser			
111	220	225	230	235
113	ctg cgg gac cag ctt cta gtt acc att cag aaa aca ttt aat tac agc	1073		
114	Leu Arg Asp Gln Leu Val Thr Ile Gln Lys Thr Phe Asn Tyr Ser			
115	240	245	250	
117	aag tcc cag tog tat cag ctg ttt gca att atc atg gag tgc atg aag	1121		
118	Lys Ser Gln Ser Tyr Gln Leu Phe Ala Ile Ile Met Glu Cys Met Lys			
119	255	260	265	
121	aag aaa gaa ctc gtc act gtg ttt cgg atg ggt tcc gag ggt cag caa	1169		
122	Lys Lys Glu Leu Val Thr Val Phe Arg Met Gly Ser Glu Gly Gln Gln			
123	270	275	280	
125	gat gtc gag atg gca att tta act gcc ttg ctc aaa gga acc aac gca	1217		
126	Asp Val Glu Met Ala Ile Leu Thr Ala Leu Leu Lys Gly Thr Asn Ala			
127	285	290	295	
129	tca gct cca gat cag ctg agc ttg gcc ctg gct tgg aac cgg gtc gac	1265		
130	Ser Ala Pro Asp Gln Leu Ser Leu Ala Leu Ala Trp Asn Arg Val Asp			
131	300	305	310	315

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133	ata gcg cga agc cag atc ttc gtc ttt ggc cca cac tgg ccg cca ctg	1313
134	Ile Ala Arg Ser Gln Ile Phe Val Phe Gly Pro His Trp Pro Pro Leu	
135	320 325 330	
137	gga agc ctg gcc cct cct gtg gac acc aaa gcc gca gag aag gaa aag	1361
138	Gly Ser Leu Ala Pro Pro Val Asp Thr Lys Ala Ala Glu Lys Glu Lys	
139	335 340 345	
141	aag cca ccc aca gcc acc acc aag ggg aga gga aaa gga aaa ggc aag	1409
142	Lys Pro Pro Thr Ala Thr Thr Lys Gly Arg Gly Lys Gly Lys Gly Lys	
143	350 355 360	
145	aag aaa ggc aaa gtg aaa gag gaa gtg gag gaa gag acg gac ccc cgg	1457
146	Lys Lys Gly Lys Val Lys Glu Glu Val Glu Glu Glu Thr Asp Pro Arg	
147	365 370 375	
149	aag ctt gag ctg ctc aac tgg gtg aat gcc ctg gag caa gcc atg ctg	1505
150	Lys Leu Glu Leu Leu Asn Trp Val Asn Ala Leu Glu Gln Ala Met Leu	
151	380 385 390 395	
153	gat gct ctt gtc cta gat cgg gtg gac ttt gta aag ctc ctg att gaa	1553
154	Asp Ala Leu Val Leu Asp Arg Val Asp Phe Val Lys Leu Leu Ile Glu	
155	400 405 410	
157	aac gga gtg aac atg cag cat ttc ctc acc atc ccg agg ctg gag gag	1601
158	Asn Gly Val Asn Met Gln His Phe Leu Thr Ile Pro Arg Leu Glu Glu	
159	415 420 425	
161	cta tac aac acc aga ctg ggc cca cca aac acc ctt cat ctg ctg gtg	1649
162	Leu Tyr Asn Thr Arg Leu Gly Pro Pro Asn Thr Leu His Leu Leu Val	
163	430 435 440	
165	cgg gat gta aag aag agc aac ctt cca cct gat tac cac atc agc ctc	1697
166	Arg Asp Val Lys Lys Ser Asn Leu Pro Pro Asp Tyr His Ile Ser Leu	
167	445 450 455	
169	att gat ata gga ctg gtg ctg gag tac ctc atg ggc ggt gcc tac cgc	1745
170	Ile Asp Ile Gly Leu Val Leu Glu Tyr Leu Met Gly Gly Ala Tyr Arg	
171	460 465 470 475	
173	tgc aac tac act cgg aaa agc ttc cgg act ctc tac aac aac ttg ttt	1793
174	Cys Asn Tyr Thr Arg Lys Ser Phe Arg Thr Leu Tyr Asn Asn Leu Phe	
175	480 485 490	
177	ggc cct aag agg gta gag ctc agc aga cac aca gtg tcc tgt gcc tcc	1841
178	Gly Pro Lys Arg Val Glu Leu Ser Arg His Thr Val Ser Cys Ala Ser	
179	495 500 505	
181	cag agt aac atg tgg ttc ctt gat gtg ctt ccc caa aag ccc acc tgt	1889
182	Gln Ser Asn Met Trp Phe Leu Asp Val Leu Pro Gln Lys Pro Thr Cys	
183	510 515 520	
185	gca gaa tgc aac tct tca cct cac ctg tcc caa act gac atc acc cca	1937
186	Ala Glu Cys Asn Ser Ser Pro His Leu Ser Gln Thr Asp Ile Thr Pro	
187	525 530 535	
189	cct ctg ccc tgacacccag tgcagggcct cctagctttc acatgcagcc	1986
190	Pro Leu Pro	
191	540	
193	attcacatcg cctctcaaga ctgggcccagg cagtgcaccc tgtcaagcat gtctgtcctc	2046
194	ccctccttcc tacaatagcc cccctctgg gccccatgcc tctgctctct cagcccgttc	2106
195	tcctccccac tgatcactgg cgctcctggt gtcttccaag gcaaggaaca aggaaaagca	2166
196	tctttttgcc cacaaaagtt tagggctccc cgctgttcaa ccatagccaa cctcactgta	2226

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197 catcggagtc atccaggcca gctgccacac acaagccttc cccaccctat cccaatagac 2286
198 cctattcctc catcaaaatc aaagctaact cctggcctgc cacattgctt cttcttgctc 2346
199 cagcctgtta aacctccaat aaatgtcaga tctgtgggaa gccttcctca ctctcactcc 2406
200 acagtttgta cagagagcga gagcctcggt tggttctact tacaaggaag gctttgtgtc 2466
201 tgtctgtcct tcccaactga cttctgttga cagaagcagt ttccacatga aagcggtgac 2526
202 tcacctggat gttgtcatta attaatagtg atacaaaata ttgacacttc ttttcctgct 2586
203 tctttgttat gcagccgaaa gcaactaagc ttctgggaat ggaagtaagt aggacatggt 2646
204 tgtggcagtt tatttactat atataccttt gtcattctgt ggaagcaaaa attgcaatgt 2706
205 tttccatgaa taaagctcgt gcc 2729
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208 <211> LENGTH: 542
209 <212> TYPE: PRT
210 <213> ORGANISM: Mus musculus
212 <400> SEQUENCE: 3
213 Met Tyr Ile Arg Val Ser Tyr Asp Thr Lys Pro Asp Ser Leu Leu His
214 1 5 10 15
215 Leu Met Val Lys Asp Trp Gln Leu Glu Leu Pro Lys Leu Leu Ile Ser
216 20 25 30
217 Val His Gly Gly Leu Gln Ser Phe Glu Met Gln Ser Lys Leu Lys Gln
218 35 40 45
219 Val Phe Gly Lys Gly Leu Ile Lys Ala Ala Met Thr Thr Gly Ala Trp
220 50 55 60
221 Ile Phe Thr Gly Gly Val Ser Thr Gly Val Val Ser His Val Gly Asp
222 65 70 75 80
223 Ala Leu Lys Asp His Ser Ser Lys Ser Arg Gly Arg Leu Cys Ala Ile
224 85 90 95
225 Gly Ile Ala Pro Trp Gly Met Val Glu Asn Lys Glu Asp Leu Ile Gly
226 100 105 110
227 Lys Asp Val Thr Arg Val Tyr Gln Thr Met Ser Asn Pro Leu Ser Lys
228 115 120 125
229 Leu Ser Val Leu Asn Asn Ser His Thr His Phe Ile Leu Ala Asp Asn
230 130 135 140
231 Gly Thr Leu Gly Lys Tyr Gly Ala Glu Val Lys Leu Arg Arg Gln Leu
232 145 150 155 160
233 Glu Lys His Ile Ser Leu Gln Lys Ile Asn Thr Arg Leu Gly Gln Gly
234 165 170 175
235 Val Pro Val Val Gly Leu Val Val Glu Gly Gly Pro Asn Val Val Ser
236 180 185 190
237 Ile Val Leu Glu Tyr Leu Lys Glu Asp Pro Pro Val Pro Val Val Val
238 195 200 205
239 Cys Asp Gly Ser Gly Arg Ala Ser Asp Ile Leu Ser Phe Ala His Lys
240 210 215 220
241 Tyr Cys Asp Glu Gly Gly Val Ile Asn Glu Ser Leu Arg Asp Gln Leu
242 225 230 235 240
243 Leu Val Thr Ile Gln Lys Thr Phe Asn Tyr Ser Lys Ser Gln Ser Tyr
244 245 250 255
245 Gln Leu Phe Ala Ile Ile Met Glu Cys Met Lys Lys Lys Glu Leu Val
246 260 265 270
247 Thr Val Phe Arg Met Gly Ser Glu Gly Gln Gln Asp Val Glu Met Ala

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248          275          280          285
249 Ile Leu Thr Ala Leu Leu Lys Gly Thr Asn Ala Ser Ala Pro Asp Gln
250          290          295          300
251 Leu Ser Leu Ala Leu Ala Trp Asn Arg Val Asp Ile Ala Arg Ser Gln
252 305          310          315          320
253 Ile Phe Val Phe Gly Pro His Trp Pro Pro Leu Gly Ser Leu Ala Pro
254          325          330          335
255 Pro Val Asp Thr Lys Ala Ala Glu Lys Glu Lys Lys Pro Pro Thr Ala
256          340          345          350
257 Thr Thr Lys Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys Gly Lys Val
258          355          360          365
259 Lys Glu Glu Val Glu Glu Glu Thr Asp Pro Arg Lys Leu Glu Leu Leu
260          370          375          380
261 Asn Trp Val Asn Ala Leu Glu Gln Ala Met Leu Asp Ala Leu Val Leu
262 385          390          395          400
263 Asp Arg Val Asp Phe Val Lys Leu Leu Ile Glu Asn Gly Val Asn Met
264          405          410          415
265 Gln His Phe Leu Thr Ile Pro Arg Leu Glu Glu Leu Tyr Asn Thr Arg
266          420          425          430
267 Leu Gly Pro Pro Asn Thr Leu His Leu Leu Val Arg Asp Val Lys Lys
268          435          440          445
269 Ser Asn Leu Pro Pro Asp Tyr His Ile Ser Leu Ile Asp Ile Gly Leu
270          450          455          460
271 Val Leu Glu Tyr Leu Met Gly Gly Ala Tyr Arg Cys Asn Tyr Thr Arg
272 465          470          475          480
273 Lys Ser Phe Arg Thr Leu Tyr Asn Asn Leu Phe Gly Pro Lys Arg Val
274          485          490          495
275 Glu Leu Ser Arg His Thr Val Ser Cys Ala Ser Gln Ser Asn Met Trp
276          500          505          510
277 Phe Leu Asp Val Leu Pro Gln Lys Pro Thr Cys Ala Glu Cys Asn Ser
278          515          520          525
279 Ser Pro His Leu Ser Gln Thr Asp Ile Thr Pro Pro Leu Pro
280          530          535          540
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283 <211> LENGTH: 20
284 <212> TYPE: DNA
285 <213> ORGANISM: Artificial Sequence
287 <220> FEATURE:
288 <223> OTHER INFORMATION: primer
290 <400> SEQUENCE: 4
291 ggggaagcac atcaaggaac
293 <210> SEQ ID NO: 5
294 <211> LENGTH: 23
295 <212> TYPE: DNA
296 <213> ORGANISM: Artificial Sequence
298 <220> FEATURE:
299 <223> OTHER INFORMATION: primer
301 <400> SEQUENCE: 5
302 gcaactacta cactcgaaa agc

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09892942.txt

Output Set: N:\CRF3\10162001\I892942.raw

L:314 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:907 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:907 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8